

Scientific Commentary

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Genomic Interpretation and Phylogenetic Analysis: Exploring the Origins and Diversity of Hawaiian Mint Species

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Published on April 10, 2024, by the Department of Biological Sciences at the State University of New York at Buffalo, the School of Biological Sciences at Nanyang Technological University, Singapore, and the Faculty of Biological and Environmental Sciences at the University of Helsinki, Finland, the research findings were published in the journal Nature Communications. Crystal M. Tomlin is the lead author, with Victor A. Albert and Charlotte Lindqvist as corresponding authors. The article is titled “Allopolyploid origin and diversification of the Hawaiian endemic mints”. The study was funded by the School of Biological Sciences at Nanyang Technological University, the National Science Foundation (2139311; 2030871), and the Research Council of Norway (154145). The research produced a chromosome-level reference genome for a representative species, ‘*Stenogyne calaminthoides*’, and resequenced its 45 close relatives. The study found that these plants evolved through multiple polyploidization events, including an allopolyploid event directly related to North American ancestors, leading to the radiation and diversification of this group in the Hawaiian Islands.

1 Interpretation of Experimental Data

Detailed genomic information about *Stenogyne calaminthoides* and its related species also revealed their complex interactions and diversification strategies during evolution.

Figure 1 describes the assembly and structural evolution of the *Stenogyne calaminthoides* genome in detail. Part (a) displays a physical photograph of the species, providing a visual reference for species morphology. Part (b)’s Hi-C contact map, marked with blue-framed chromosomes, shows the interactions and spatial structure between chromosomes, providing key information for understanding the three-dimensional structure of the genome. Part (c) reveals the distribution of genes and various types of repetitive sequences (such as Copia, Helitron, Gypsy) in the genome, displaying density per 1 Mb area and highlighting homologous regions with different colors, enhancing our understanding of genomic complexity. Part (d) compares the *S. calaminthoides* genome with grape chromosomes through a fractional deviation plot, showing conservation and variation in genome evolution. Part (e)’s phylogenetic tree discusses the history of polyploidy events within the genus *Stenogyne*, including unique whole-genome duplication events, which are crucial for understanding their adaptive evolution.

Figure 2 depicts the phylogenetic relationships and genetic admixture among Hawaiian mint species and their related groups through two types of phylogenetic trees. The tree on the left is based on a dataset of single nucleotide polymorphisms (SNPs) and analyzed using a maximum likelihood approach, while the tree on the right is based on the coalescent analysis of single-copy nuclear genes, each highlighting the evolutionary relationships and gene flow among species. The figure also includes an ADMIXTURE analysis, which reveals the gene flow and diversity of genetic backgrounds among species, with each color representing different ancestral populations, thus illustrating the complex dynamics of genetic mixing and species formation.

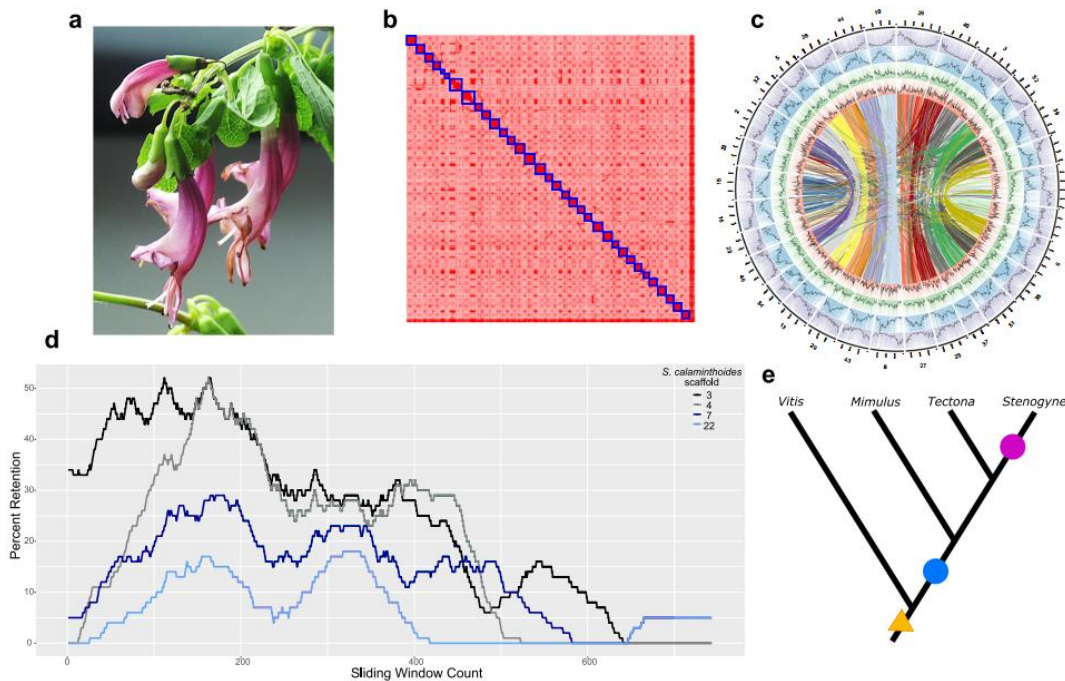


Figure 1 Assembly and structural evolution of the *Stenogyne calaminthoides* genome

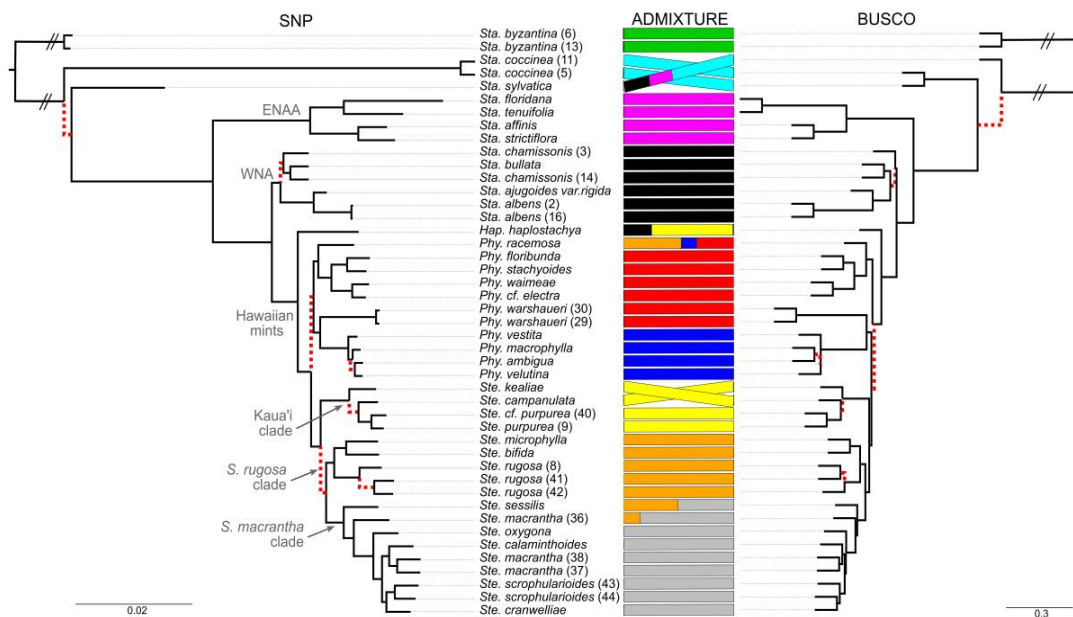


Figure 2 Phylogenetic relationships and admixture among Hawaiian mints and relatives

2 Insight into Research Findings

The research conducted an in-depth exploration of the origins and evolutionary history of Hawaiian mints through genome size prediction, chromosome assembly quality assessment, repetitive sequence analysis, and phylogenetic analysis. The study indicates that geographical isolation and genetic drift in small populations played a major role in species formation, while local mixed mating may have also played a significant role in early lineage diversity.

3 Evaluation of the Research

This research utilized high-quality genomic data and advanced analytical methods, providing valuable insights into the formation of island biodiversity. However, direct evidence for specific adaptive traits and niche differentiation remains insufficient, areas that future research could further explore.

4 Concluding Remarks

The study demonstrates that Hawaiian mint species have adapted to the unique ecological environment of the Hawaiian Islands through a series of complex evolutionary processes, including allopolyploidy and interspecies hybridization. These processes provide a genomic basis for species ecological adaptation and morphological diversity.

5 Access the Full Text

Tomlin C.M., Rajaraman S., Sebesta J.T., et al., Allopolyploid origin and diversification of the Hawaiian endemic mints, Nat Commun 15, 3109 (2024). <https://doi.org/10.1038/s41467-024-47247-y>.

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